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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/898,570

DATE: 11/13/2001
TIME: 14:55:33

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3 <110> APPLICANT: GERLACH, VALERIE L.
4 ELLERMAN, KAREN
5 MACDOUGALL, JOHN R.
6 SMITHSON, GLENNDA
8 <120> TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND
9 METHODS OF USING THE SAME
11 <130> FILE REFERENCE: 15966-776CIP
13 <140> CURRENT APPLICATION NUMBER: 09/898,570
14 <141> CURRENT FILING DATE: 2001-07-03
16 <150> PRIOR APPLICATION NUMBER: 60/198,293
17 <151> PRIOR FILING DATE: 2000-04-19
19 <150> PRIOR APPLICATION NUMBER: 60/198,645
20 <151> PRIOR FILING DATE: 2000-04-20
22 <150> PRIOR APPLICATION NUMBER: 60/210,809
23 <151> PRIOR FILING DATE: 2000-06-09
25 <150> PRIOR APPLICATION NUMBER: 60/199,476
26 <151> PRIOR FILING DATE: 2000-04-26
28 <150> PRIOR APPLICATION NUMBER: 60/200,025
29 <151> PRIOR FILING DATE: 2000-04-26
31 <150> PRIOR APPLICATION NUMBER: 60/224,610
32 <151> PRIOR FILING DATE: 2000-08-11
34 <150> PRIOR APPLICATION NUMBER: 60/200,024
35 <151> PRIOR FILING DATE: 2000-04-26
37 <150> PRIOR APPLICATION NUMBER: 60/199,880
38 <151> PRIOR FILING DATE: 2000-04-26
40 <150> PRIOR APPLICATION NUMBER: 60/218,591
41 <151> PRIOR FILING DATE: 2000-07-17
43 <150> PRIOR APPLICATION NUMBER: 60/271,814
44 <151> PRIOR FILING DATE: 2001-02-27
46 <150> PRIOR APPLICATION NUMBER: 60/215,855
47 <151> PRIOR FILING DATE: 2000-07-03
49 <150> PRIOR APPLICATION NUMBER: 09/839,446
50 <151> PRIOR FILING DATE: 2001-04-19
52 <160> NUMBER OF SEQ ID NOS: 58
54 <170> SOFTWARE: PatentIn Ver. 2.1
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58 <212> TYPE: DNA
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62 <223> OTHER INFORMATION: Description of Unknown Organism: POLYX
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68 atgaaacaaa cctggatgca agaaactaga atgaagaaag atgacagtac caaagcgcgg 180
69 cctcagaaat atgagcaact tctccatata gaggacaacg atttcgcaat gagacctgga 240

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79 tcatcagcat ttattggaca tctactgttt ttgatctgga gttccaggaa aagaccaggt 840
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95 caataattca aagatatttt gttcttagt gccagccaag tgccctggta tctaccagag 1800
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105 <220> FEATURE:

106 <223> OTHER INFORMATION: Description of Unknown Organism: POLYX

107 GM_83055392_A

110 <400> SEQUENCE: 2

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114 Leu Lys Pro Asn Val Cys Ala Ala Ser Asn Ile Lys Met Thr His Gln
115           20           25           30
117 Arg Cys Ser Ser Ser Met Lys Gln Thr Trp Met Gln Glu Thr Arg Met
118           35           40           45
120 Lys Lys Asp Asp Ser Thr Lys Ala Arg Pro Gln Lys Tyr Glu Gln Leu
121           50           55           60
123 Leu His Ile Glu Asp Asn Asp Phe Ala Met Arg Pro Gly Phe Gly Gly
124           65           70           75           80
126 Ser Pro Val Pro Val Gly Ile Asp Val His Val Glu Ser Ile Asp Ser
127           85           90           95
129 Ile Ser Glu Thr Asn Met Asp Phe Thr Met Thr Phe Tyr Leu Arg His

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132 Tyr Trp Lys Asp Glu Arg Leu Ser Phe Pro Ser Thr Ala Asn Lys Ser
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135 Met Thr Phe Asp His Arg His Leu Arg Tyr Ser Leu Phe Ile Arg Arg
136          130          135          140
138 Leu Tyr Leu Leu Tyr Cys Gln Arg Ser Phe Phe Ser Pro Ser Ser Ile
139 145          150          155          160
141 Leu Pro Ser Ser Pro Asp Ile His Ala Pro Gly Thr Ser Lys Ser Ser
142          165          170          175
144 Leu Ser Asp Ser Leu Val Cys Ile Ser Glu Lys Asn Leu Pro Gly His
145          180          185          190
147 Ser Lys Asn Thr Pro Leu Ala Met Ser Asp Val Ala Tyr Asn Glu Asp
148          195          200          205
150 Asp Leu Met Leu Tyr Trp Lys His Gly Asn Lys Ser Leu Asn Thr Glu
151          210          215          220
153 Glu His Met Ser Leu Ser Gln Phe Phe Ile Glu Asp Phe Ser Ala Ser
154 225          230          235          240
156 Ser Gly Leu Ala Phe Tyr Ser Ser Thr Gly Thr Ala Phe Tyr Met Gly
157          245          250          255
159 Asp Ser Ser Ala Phe Ile Gly His Leu Leu Phe Leu Ile Trp Ser Ser
160          260          265          270
162 Arg Lys Arg Pro Gly Leu Glu Met Leu Gly Leu Gly Ile Leu Arg Ile
163          275          280          285
165 Trp Val Ile Thr Arg Ala Met Asp Lys Lys Met Glu Met Gly Ile Thr
166          290          295          300
168 Thr Val Leu Thr Met Ser Thr Ile Ile Thr Ala Val Ser Ala Ser Met
169 305          310          315          320
171 Pro Gln Val Ser Tyr Leu Lys Ala Val Asp Val Tyr Leu Trp Val Ser
172          325          330          335
174 Ser Leu Phe Val Phe Leu Ser Val Ile Glu Tyr Ala Ala Val Asn Tyr
175          340          345          350
177 Leu Thr Thr Val Glu Glu Arg Lys Gln Phe Lys Lys Ser Phe Ser Lys
178          355          360          365
180 Ile Ser Arg Met Tyr Asn Ile Asp Ala Val Gln Ala Met Ala Phe Asp
181          370          375          380
183 Gly Cys Tyr His Asp Ser Glu Ile Asp Met Asp Gln Thr Ser Leu Ser
184 385          390          395          400
186 Leu Asn Ser Glu Asp Phe Met Arg Arg Lys Ser Ile Cys Ser Pro Ser
187          405          410          415
189 Thr Asp Ser Ser Arg Ile Lys Arg Arg Lys Ser Leu Gly Gly His Val
190          420          425          430
192 Gly Arg Ile Ile Leu Glu Asn Asn His Val Ile Asp Thr Tyr Ser Arg
193          435          440          445
195 Ile Leu Phe Pro Ile Val Tyr Ile Phe Phe Asn Leu Phe Tyr Trp Gly
196          450          455          460
198 Val Tyr Val
199 465
202 <210> SEQ ID NO: 3
203 <211> LENGTH: 1417

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204 <212> TYPE: DNA
205 <213> ORGANISM: Unknown Organism
207 <220> FEATURE:
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214 cagcaaacaa gaaactagaa tgaagaaaga tgacagtacc aaagcgcggc ctcagaaata 180
215 tgagcaactt ctccatatag aggacaacga ttctgcaatg agacctggat ttggagggttc 240
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226 gatgatgctt tcatgggttt ctttttggat tgaccgaaga gctgttctct caagagtttc 900
227 cctgggaatc accacagtgc tgaccatgtc cacaatcacc actgctgtga gcgcctccat 960
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251 Leu Val Cys Ala Ala Ser Asn Ile Lys Met Thr His Gln Arg Cys Ser
252             20             25             30
254 Ser Ser Met Lys Gln Thr Ser Lys Gln Glu Thr Arg Met Lys Lys Asp
255             35             40             45
257 Asp Ser Thr Lys Ala Arg Pro Gln Lys Tyr Glu Gln Leu Leu His Ile
258             50             55             60
260 Glu Asp Asn Asp Phe Ala Met Arg Pro Gly Phe Gly Gly Ser Pro Val
261 65             70             75             80
263 Pro Val Gly Ile Asp Val His Val Glu Ser Ile Asp Ser Ile Ser Glu

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264          85          90          95
266 Thr Asn Met Asp Phe Thr Met Thr Phe Tyr Leu Arg His Tyr Trp Lys
267          100          105          110
269 Asp Glu Arg Leu Ser Phe Pro Ser Thr Ala Asn Lys Ser Met Thr Phe
270          115          120          125
272 Asp His Arg Leu Thr Arg Lys Ile Trp Val Pro Asp Ile Phe Phe Val
273          130          135          140
275 His Ser Lys Arg Ser Phe Ile His Asp Thr Thr Met Glu Asn Ile Met
276 145          150          155          160
278 Leu Arg Val His Pro Asp Gly Asn Val Leu Leu Ser Leu Arg Ile Thr
279          165          170          175
281 Val Ser Ala Met Cys Phe Met Asp Phe Ser Arg Phe Pro Leu Asp Thr
282          180          185          190
284 Gln Asn Cys Ser Leu Glu Leu Glu Ser Ala Tyr Asn Glu Asp Asp Leu
285          195          200          205
287 Met Leu Tyr Trp Lys His Gly Asn Lys Ser Leu Asn Thr Glu Glu His
288 210          215          220
290 Met Ser Leu Ser Gln Phe Ile Glu Asp Phe Ser Ala Ser Ser Gly
291 225          230          235          240
293 Leu Ala Phe Tyr Ser Ser Thr Thr Gly Trp Tyr Asn Arg Leu Phe Ile
294          245          250          255
296 Ile Ser Val Leu Arg Arg His Val Phe Phe Phe Val Leu Pro Thr Tyr
297          260          265          270
299 Phe Pro Ala Ile Leu Met Val Met Leu Ser Trp Val Ser Phe Trp Ile
300          275          280          285
302 Asp Arg Arg Ala Val Pro Ala Arg Val Ser Leu Gly Ile Thr Thr Val
303 290          295          300
305 Leu Thr Met Ser Thr Ile Ile Thr Ala Val Ser Ala Ser Met Pro Gln
306 305          310          315          320
308 Val Ser Tyr Leu Lys Ala Val Asp Val Tyr Leu Trp Val Ser Ser Leu
309          325          330          335
311 Phe Val Phe Leu Ser Val Ile Glu Tyr Ala Ala Val Asn Tyr Leu Thr
312          340          345          350
314 Thr Val Glu Glu Arg Lys Gln Phe Lys Lys Thr Gly Lys Ile Ser Arg
315          355          360          365
317 Met Tyr Asn Ile Asp Ala Val Gln Ala Met Ala Phe Asp Gly Cys Tyr
318          370          375          380
320 His Asp Ser Glu Ile Asp Met Asp Gln Thr Ser Leu Ser Leu Asn Ser
321 385          390          395          400
323 Glu Asp Phe Met Arg Arg Lys Ser Ile Cys Ser Pro Ser Thr Asp Ser
324          405          410          415
326 Ser Arg Ile Lys Arg Arg Lys Ser Leu Gly Gly His Val Gly Arg Ile
327          420          425          430
329 Ile Leu Glu Asn Asn His Val Ile Asp Thr Tyr Ser Arg Ile Leu Phe
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340 <211> LENGTH: 1444

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/898,570

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